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(54) Title: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING SAME, AND METHODS OF USE

(57) Abstract: The present invention relates to clusters of plant genes that areregulated in response to one or more stress conditions. The present invention also relates to isolated plant stress-regulated genes, including portions thereof comprising a coding sequence or a regulatory element, and to consensus sequences comprising a plant stress-regulated regulatory element. In addition, the invention relates to a recombinant polynucleotide, which includes a plant stress-regulated gene, or functional portion thereof, operatively linked to a heterologous mucleotide sequence. The invention further relates to a transgenic plant, which contains a plant stress-regulated gene or functional portion thereof that was introduced into a progenitor cell of the plant. In addition, the invention relates to methods of using a plant stress-regulated gene to confer upon a plant a selective advantage to a stress condition. The invention also relates to a method of identifying an agent that modulates the activity of a plant stress-regulated regulatory element.

STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING SAME, AND METHODS OF USE

BACKGROUND OF THE INVENTION

FIELD OF THE INVENTION

The present invention relates generally to plant genes, the expression of which are regulated in response to stress, and more specifically to the gene regulatory elements involved in a stress-induced response in plants, to uses of the coding sequences and regulatory elements of such plant stress-regulated genes, and to transgenic plants genetically modified to express such a coding sequence or to express a heterologous polynucleotide from such a regulatory element.

BACKGROUND INFORMATION

Microarray technology is a powerful tool that can be used to identify the presence and level of expression of a large number of polynucleotides in a single assay. A microarray is formed by linking a large number of discrete polynucleotide sequences, for example, a population of polynucleotides representative of a genome of an organism, to a solid support such as a microchip, glass slide, or the like, in a defined pattern. By contacting the microarray with a nucleic acid sample obtained from a cell of interest, and detecting those polynucleotides expressed in the cell can hybridize specifically to complementary sequences on the chip, the pattern formed by the hybridizing polynucleotides allows the identification of clusters of genes that are expressed in the cell. Furthermore, where each polynucleotide linked to the solid support is known, the identity of the hybridizing sequences from the nucleic acid sample can be identified.

A strength of microarray technology is that it allows the identification of differential gene expression simply by comparing patterns of hybridization. For example, by comparing the hybridization pattern of nucleic acid molecules obtained from cells of an individual suffering from a disease with the nucleic acids obtained from the corresponding cells of a healthy individual, genes that are differentially expressed can be identified. The identification of such differentially expressed genes

provides a means to identify new genes, and can provide insight as to the etiology of a disease.

Microarray technology has been widely used to identify patterns of gene expression associated with particular stages of development or of disease conditions in animal model systems, and is being applied to the identification of specific patterns of gene expression in humans. The recent availability of information for the genomes of plants provides a means to adapt microarray technology to the study of plant gene expression.

Plants and plant products provide the primary sustenance, either directly or indirectly, for all animal life, including humans. For the majority of the world's human population and for many animals, plants and plant products provide the sole source of nutrition. As the world population increases, the best hope to prevent widespread famine is to increase the quantity and improve the quality of food crops, and to make the crops available to the regions of the world most in need of food.

Throughout history, a continual effort has been made to increase the yield and nutritious value of food crops. For centuries, plants having desirable characteristics such as greater resistance to drought conditions or increased size of fruit were crossbred and progeny plants exhibiting the desired characteristics were selected and used to produce seed or cuttings for propagation. Using such classical genetic methods, plants having, for example, greater disease resistance, increased yield, and better flavor have been obtained. The identification of plant genes involved in conferring a selective advantage on the plant to an environmental challenge would facilitate the generation and yield of plants, thereby increasing the available food supply to an increasing world population. The involvement of these genes in a single organism to responses to multiple stress conditions, however, remains unknown. Thus, a need exists to identify plant genes and polynucleotides that are involved in modulating the response of a plant to changing environmental conditions. The present invention satisfies this need and provides additional advantages.

SUMMARY OF THE INVENTION

The present invention relates to clusters of genes that are regulated in response to a stress condition in plants. Such clusters include, for example, plant polynucleotides

whose expression is altered in response to two or more different stress conditions; and plant polynucleotides the expression of which are altered in response to one stress condition, but not to others. The identification of such clusters, using microarray technology, has allowed the identification of plant stress-regulated genes in *Arabidopsis thaliana* (see Tables 1 and 2); and homologs and orthologs thereof in other plant species (see Table 32). Thus, the invention provides isolated polynucleotide portions of *Arabidopsis* plant stress-regulated genes, and homologs and orthologs thereof; variants of such sequences, and polynucleotides encoding substantially similar plant stress-regulated polypeptides expressed therefrom. Such sequences include, for example, sequences encoding transcription factors; enzymes, including kinases; and structural proteins, including channel proteins (see Tables 29-31). Accordingly, the present invention also relates to an isolated polynucleotide comprising all or a portion of a plant stress-regulated gene, and to polynucleotide portions thereof, including a coding region (open reading frame), which encodes all or a portion of a stress-regulated polypeptide, for example, as set forth in SEQ ID NOS:1-2703; and a regulatory element involved in regulating the response of the plant to a stress condition such exposure to an abnormal level of salt, osmotic pressure, temperature or any combination thereof, for example, as set forth in SEQ ID NOS:2704-5379.

The present invention also relates to a recombinant polynucleotide, which contains a nucleotide sequence of a plant stress-regulated gene or functional portion thereof operatively linked to a heterologous nucleotide sequence. In one embodiment, the recombinant polynucleotide comprises a plant stress-regulated gene regulatory element operatively linked to a heterologous nucleotide sequence, which is not regulated by the regulatory element in a naturally occurring plant. The heterologous nucleotide sequence, when expressed from the regulatory element, can confer a desirable phenotype to a plant cell containing the recombinant polynucleotide. In another embodiment, the recombinant polynucleotide comprises a coding region, or portion thereof, of a plant stress-regulated gene operatively linked to a heterologous promoter. The heterologous promoter provides a means to express an encoded stress-regulated polypeptide constitutively, or in a tissue-specific or phase-specific manner.

Accordingly, in one aspect, the present invention provides an isolated polynucleotide comprising a nucleotide sequence of a plant gene that hybridizes under

stringent conditions, preferably high stringency conditions, to any one of SEQ ID NOS:1-5379 (see Tables 1 and 2), including to a coding region (SEQ ID NOS:1-2703) or a regulatory region, which can alter transcription of an operatively linked nucleic acid sequence in response to an abiotic stress (SEQ ID NOS:2704-5379; see Table 2), or to a complement thereof. Additional aspects provide sequences that hybridize under stringent conditions, preferably high stringency conditions, to the complements of SEQ ID NO 1-1261 (cold responsive genes; Tables 3-6), SEQ ID NOS:2227-2427 (saline responsive genes; Tables 7-10), SEQ ID NOS:2428-2585 (osmotic responsive genes; Tables 11-14), SEQ ID NOS:1699-1969 (cold and osmotic responsive genes; Tables 15-17), SEQ ID NOS:1970-2226 (cold and saline responsive genes; Tables 18-20), SEQ ID NOS:2586-2703 (osmotic and saline responsive genes; Tables 21-23), and SEQ ID NOS:1262-1698(cold, osmotic and saline responsive genes; Tables 24-26), and which can comprise regulatory regions that can alter transcription in response to cold stress, osmotic stress, saline stress, or combinations thereof (SEQ ID NOS:2704-5379; see Table 2). Also provided are nucleotide sequences complementary thereto, and expression cassettes, plants and seeds comprising any of the above isolated sequences.

In another aspect, the present invention provides an isolated polynucleotide comprising a plant nucleotide sequence that hybridizes under stringent conditions, preferably high stringency conditions, to the complement of any one of SEQ ID NOS:1-2703 (Table 1), including to a coding region thereof (SEQ ID NOS:2704-5379), wherein expression of said coding region is altered in response to an abiotic stress. Additional aspects provide sequences that hybridize under high stringency conditions to the complements of SEQ ID NO 1-1261 (cold responsive genes; Tables 3-6), SEQ ID NOS:2227-2427 (saline responsive genes; Tables 7-10), SEQ ID NOS:2428-2585 (osmotic responsive genes; Tables 11-14), SEQ ID NOS:1699-1969 (cold and osmotic responsive genes; Tables 15-17), SEQ ID NOS:1970-2226 (cold and saline responsive genes; Tables 18-20), SEQ ID NOS:2586-2703 (osmotic and saline responsive genes; Tables 21-23), and SEQ ID NOS:1262-1698(cold, osmotic and saline responsive genes; Tables 24-26), and which can comprise a coding region whose transcription is altered in response to cold stress, osmotic stress, saline stress, or a combination thereof. Also provided are nucleotide

sequences complementary thereto, and expression cassettes, plants and seeds comprising any of the above sequences.

The invention further relates to a method of producing a transgenic plant, which comprises at least one plant cell that exhibits altered responsiveness to a stress condition. In one embodiment, the method can be performed by introducing a polynucleotide portion of plant stress-regulated gene into a plant cell genome, whereby the polynucleotide portion of the plant stress-regulated gene modulates a response of the plant cell to a stress condition.

The polynucleotide portion of the plant stress-regulated gene can encode a stress-regulated polypeptide or functional peptide portion thereof (see SEQ ID NOS:1-2703), wherein expression of the stress-regulated polypeptide or functional peptide portion thereof either increases the stress tolerance of the transgenic plant, or decreases the stress tolerance of the transgenic plant. The polynucleotide portion of the plant stress-regulated gene encoding the stress-regulated polypeptide or functional peptide portion thereof can be operatively linked to a heterologous promoter. The polynucleotide portion of the plant stress-regulated gene also can comprise a stress-regulated gene regulatory element (see SEQ ID NOS:2704-5379). The stress-regulated gene regulatory element can integrate into the plant cell genome in a site-specific manner, whereupon it can be operatively linked to a heterologous nucleotide sequence, which can be expressed in response to a stress condition specific for the regulatory element; or can be a mutant regulatory element, which is not responsive to the stress condition, whereby upon integrating into the plant cell genome, the mutant regulatory element disrupts an endogenous stress-regulated regulatory element of a plant stress-regulated gene, thereby altering the responsiveness of the plant stress-regulated gene to the stress condition.

In one aspect, the invention provides a method for producing a transgenic plant by introducing into at least one plant cell a recombinant nucleic acid construct comprising i) all or a portion of any one of SEQ ID NOS:1-5379; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to all or a portion of the complement of any one of SEQ ID NOS:1-2703; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to abiotic stress, and that hybridizes under conditions of

high stringency to the complement of any one of SEQ ID NOS:2704-5379; iv) a polynucleotide having at least 90% sequence identity with any one of SEQ ID NO:1-5379; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv), wherein the fragment comprises a nucleotide sequence that alters transcription of an operatively linked coding region in response to abiotic stress; and regenerating a plant from the at least one plant cell.

Another aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:1-1261 or 2704-3955; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:1-1261; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to cold stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:2704-3955; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:1-1261 or 2704-3955; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv) wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to cold stress; and regenerating a plant from the at least one plant cell.

In another aspect, the invention provides a method for producing a transgenic plant by introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:2428-2585 or 5108-5263; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:2428-2585; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to osmotic stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:5108-5263; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:2428-2585 or 5108-5263; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the

sequences of iv), wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to osmotic stress; and regenerating a plant from the at least one plant cell.

Still another aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:2227-2427 or 4910-5107; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:2227-2427; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to saline stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:2227-2427; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:4910-5107; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv) wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to saline stress; and regenerating a plant from the at least one plant cell.

Yet another aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:1699-1969 or 4389-4654; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:1699-1969; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to a combination of cold and osmotic stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:4389-4654; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:1699-1969 or 4389-4654; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv), wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to a combination of cold and osmotic stress; and regenerating a plant from the at least one plant cell.

Yet another aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:1970-2226 or 4655-4909; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:1970-2226; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to a combination of cold and saline stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:4655-4909; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:1970-2226 or 4655-4909; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv), wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to a combination of cold and saline stress; and regenerating a plant from the at least one plant cell.

A further aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:2586-2703 or 5264-5379; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:2586-2703; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to a combination of osmotic and saline stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS: 5264-5379; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:2586-2703 or 5264-5379; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv), wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to a combination of osmotic and saline stress; and regenerating a plant from the at least one plant cell.

Another aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct

What is claimed is:

1. A method of identifying a stress condition to which a plant cell has been exposed, the method comprising:

a) contacting nucleic acid molecules representative of expressed polynucleotides in the plant cell with an array of probes representative of the plant cell genome; and

b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response, thereby identifying the stress condition to which the plant cell was exposed.

2. The method of claim 1, wherein the stress condition is an abiotic stress condition.

3. The method of claim 2, wherein the abiotic stress is a cold stress condition, an osmotic stress condition, a saline stress condition, or a combination thereof.

4. The method of claim 1, wherein the profile is characteristic of exposure to a single stress condition.

5. The method of claim 1, wherein the profile is characteristic of a cold stress response, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1-155, 157-229, 230-232, 234-557, 559-572, 574-605, 607-634, 636-634, 636-786, 788-812, and 814-1261.

6. The method of claim 1, wherein the profile is characteristic of a cold stress response, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1-1261.

7. The method of claim 1, wherein the profile is characteristic of an osmotic stress response, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:2428-2585.

8. The method of claim 1, wherein the profile is characteristic of a saline stress response, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:2227-2427.

9. The method of claim 2, wherein the profile is characteristic of exposure to at least two abiotic stress conditions.

10. The method of claim 9, wherein the abiotic stress conditions are cold and osmotic stress conditions, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1699-1725, 1727-1865, 1867-1917, 1919-1927, and 1929-1969.

11. The method of claim 9, wherein the abiotic stress conditions are cold and osmotic stress conditions, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1699-1969.

12. The method of claim 9, wherein the abiotic stress conditions are cold and saline stress conditions, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1970-2226.

13. The method of claim 9, wherein the abiotic stress conditions are osmotic and saline stress conditions, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:2586-2703.

14. The method of claim 9, wherein the abiotic stress conditions are cold, osmotic and saline stress conditions, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, and 1634-1698.

15. The method of claim 9, wherein the abiotic stress conditions are cold, osmotic and saline stress conditions, and wherein the expressed polynucleotides comprise one or a plurality of SEQ ID NOS:1262-1698.

16. The method of claim 1, wherein the nucleic acid molecules representative of expressed polynucleotides in the plant cell are RNA molecules or cDNA molecules.

17. The method of claim 1, wherein the array of probes representative of the plant cell genome is immobilized on a microchip.

18. A method for determining whether a test plant has been exposed to an abiotic stress, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence,

wherein the probe comprises at least 15 nucleotides of a plant stress-regulated gene, provided said gene does not comprise a nucleotide sequence of a polynucleotide as set forth in any of SEQ ID NOS:156, 229, 233, 558, 573, 606, 635, 787, 813, 1263, 1386, 1391, 1405, 1445, 1484, 1589, 1609, 1634, 1726, 1866, 1918 or 1928,or a nucleotide sequence complementary thereto,

whereby

detecting selective hybridization of at least one nucleic acid probe, or

detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to an abiotic stress,

indicates that the test plant has been exposed to an abiotic stress, and

whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to an abiotic stress.

19. The method of claim 18, wherein the abiotic stress is cold stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1261 or a nucleotide sequence complementary thereto.

20. The method of claim 18, wherein the abiotic stress is saline stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2226-2427 or a nucleotide sequence complementary thereto.

21. The method of claim 18, wherein the abiotic stress is osmotic stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in two or more of SEQ ID NOS:2428-2585 or a nucleotide sequence complementary thereto.

22. A method for determining whether a test plant has been exposed to a cold stress, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence,

wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1261, or a nucleotide sequence complementary thereto,

whereby

detecting selective hybridization of at least one nucleic acid probe, or

detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to a cold stress,

indicates that the test plant has been exposed to a cold stress, and

whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to a cold stress.

23. A method for determining whether a test plant has been exposed to a saline stress, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence,

wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2226-2427, or a nucleotide sequence complementary thereto,

whereby

detecting selective hybridization of at least one nucleic acid probe, or

detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to a saline stress,

indicates that the test plant has been exposed to a saline stress, and

whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to a saline stress.

24. A method for determining whether a test plant has been exposed to an osmotic stress, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence,

wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in two or more of SEQ ID NOS:2428-2585, or a nucleotide sequence complementary thereto,

whereby

detecting selective hybridization of at least one nucleic acid probe, or

detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to an osmotic stress,

indicates that the test plant has been exposed to an osmotic stress, and

whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to an osmotic stress.

25. A method for determining whether a test plant has been exposed to a combination of abiotic stress conditions, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence,

whereby

detecting selective hybridization of at least one nucleic acid probe, or

detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to a combination of stress conditions,

indicates that the test plant has been exposed to a combination of abiotic stress conditions, and

whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to a combination of abiotic stress conditions.

26. The method of claim 25, wherein the combination of abiotic stress conditions is a combination of a cold stress and an osmotic stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1699-1969, or a nucleotide sequence complementary thereto.

27. The method of claim 25, wherein the combination of abiotic stress conditions is a combination of a cold stress and a saline stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1970-2226, or a nucleotide sequence complementary thereto.

28. The method of claim 25, wherein the combination of abiotic stress conditions is a combination of an osmotic stress and a saline stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2586-2703, or a nucleotide sequence complementary thereto.

29. The method of claim 25, wherein the combination of abiotic stress conditions is a combination of a cold stress, a saline stress and an osmotic stress, and wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1262-1698, or a nucleotide sequence complementary thereto.

30. A method for determining whether a test plant has been exposed to a cold stress and an osmotic stress, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence,

wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1699-1969, or a nucleotide sequence complementary thereto,

whereby

detecting selective hybridization of at least one nucleic acid probe, or

detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to a cold stress and an osmotic stress,

indicates that the test plant has been exposed to a cold stress and an osmotic stress, and

whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to a cold stress and an osmotic stress.

31. A method for determining whether a test plant has been exposed to a cold stress and a saline stress, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence,

wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1970-2226, or a nucleotide sequence complementary thereto,

whereby

detecting selective hybridization of at least one nucleic acid probe, or

detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to a cold stress and a saline stress,

indicates that the test plant has been exposed to a cold stress and a saline stress, and

whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to a cold stress and a saline stress.

32. A method for determining whether a test plant has been exposed to an osmotic stress and a saline stress, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence,

wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2586-2703, or a nucleotide sequence complementary thereto,

whereby

detecting selective hybridization of at least one nucleic acid probe, or

detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to an osmotic stress and a saline stress,

indicates that the test plant has been exposed to an osmotic stress and a saline stress, and

whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to an osmotic stress and a saline stress.

33. A method for determining whether a test plant has been exposed to a cold stress, a saline stress and an osmotic stress, the method comprising contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with a plurality of nucleic acid probes under conditions suitable for selective hybridization to a complementary nucleotide sequence,

wherein the probe comprises at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1262-1698, or a nucleotide sequence complementary thereto,

whereby

detecting selective hybridization of at least one nucleic acid probe, or

detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to a cold stress, a saline stress, and an osmotic stress,

indicates that the test plant has been exposed to a cold stress, a saline stress and an osmotic stress, and

whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to a cold stress, a saline stress and an osmotic stress.

34. A method for determining whether a test plant has been exposed to a cold stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:1-155, 157-229, 230-232, 234-557, 559-572, 574-605, 607-634, 636-634, 636-786, 788-812, and 814-1261 in cells of the test plant,

wherein

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a cold stress, or

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a cold stress,

indicates the test plant has been exposed to a cold stress, or

wherein

detecting a level of expression that is less than at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a cold stress, or

detecting a level of expression that is at least two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a cold stress,

indicates the test plant has not been exposed to a cold stress.

35. A method for determining whether a test plant has been exposed to a saline stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:2226-2427 in cells of the test plant,

wherein

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a saline stress, or

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a saline stress,

indicates the test plant has been exposed to a saline stress, or

wherein

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a saline stress, or

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a saline stress,

indicates the test plant has not been exposed to a saline stress.

36. A method for determining whether a test plant has been exposed to an osmotic stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:2428-2585 in cells of the test plant,

wherein

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to an osmotic stress, or

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to an osmotic stress,

indicates the test plant has been exposed to a osmotic stress, or

wherein

detecting a level of expression that is less than about two-fold different from level of expression of the at least one polynucleotide in cells of a plant not exposed to an osmotic stress, or

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to an osmotic stress,

indicates the test plant has not been exposed to a osmotic stress.

37. A method for determining whether a test plant has been exposed to a cold stress and an osmotic stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:1699-1969 in cells of the test plant,

wherein

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a cold stress and an osmotic stress, or

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a cold stress and an osmotic stress,

indicates the test plant has been exposed to a cold stress and an osmotic stress, or

wherein

detecting a level of expression that is less than about two-fold different from as a level of expression of the at least one polynucleotide in cells of a plant not exposed to a cold stress and an osmotic stress, or

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a cold stress and an osmotic stress,

indicates the test plant has not been exposed to a cold stress and an osmotic stress.

38. A method for determining whether a test plant has been exposed to a cold stress and a saline stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:1970-2226 in cells of the test plant,

wherein

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a cold stress and a saline stress, or

detecting a level of expression that is less than about two-fold different from as a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a cold stress and a saline stress,

indicates the test plant has been exposed to a cold stress and a saline stress, or

wherein

detecting a level of expression that is less than about two-fold different from as a level of expression of the at least one polynucleotide in cells of a plant not exposed to a cold stress and a saline stress, or

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a cold stress and a saline stress,

indicates the test plant has not been exposed to a cold stress and a saline stress.

39. A method for determining whether a test plant has been exposed to a saline stress and an osmotic stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:2586-2703 in cells of the test plant,

wherein

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a saline stress and an osmotic stress, or

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a saline stress and an osmotic stress,

indicates the test plant has been exposed to a saline stress and an osmotic stress, or

wherein

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a saline stress and an osmotic stress, or

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to saline stress and an osmotic stress,

indicates the test plant has not been exposed to a saline stress and an osmotic stress.

40. A method for determining whether a test plant has been exposed to a cold stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth SEQ ID NOS:1-155, 157-229, 230-232, 234-557, 559-572, 574-605, 607-634, 636-634, 636-786, 788-812, and 814-1261 in cells of the test plant,

wherein

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a cold stress, or

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a cold stress,

indicates the test plant has been exposed to a cold stress, or

wherein

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a cold stress, or

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a cold stress,

indicates the test plant has not been exposed to a cold stress.

41. A method for determining whether a test plant has been exposed to a cold stress, a saline stress and an osmotic stress, the method comprising detecting a level of expression of at least one polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NOS:1262-1698 in cells of the test plant,

wherein

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a cold stress, a saline stress and an osmotic stress, or

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a cold stress, a saline stress and an osmotic stress,

indicates the test plant has been exposed to a cold stress, a saline stress and an osmotic stress, or

wherein

detecting a level of expression that is less than about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant not exposed to a cold stress, a saline stress and an osmotic stress, or

detecting a level of expression that is at least about two-fold different from a level of expression of the at least one polynucleotide in cells of a plant known to be exposed to a cold stress, a saline stress and an osmotic stress,

indicates the test plant has not been exposed to a cold stress, a saline stress and an osmotic stress.

42. A method of producing a transgenic plant comprising plant cells that exhibit altered responsiveness to at least one stress condition, the method comprising introducing a polynucleotide portion of a plant stress-regulated gene into a plant cell genome, wherein the polynucleotide portion of the stress-regulated gene does not comprise a nucleotide sequence as set forth in any of SEQ ID NOS:156, 229, 233, 558, 573, 606, 635, 787, 813, 1263, 1386, 1391, 1405, 1445, 1484, 1589, 1609, 1634, 1726, 1866, 1918 or 1928, whereby the polynucleotide portion of the plant stress-regulated gene modulates a response of the plant cells to at least one stress condition, thereby producing a transgenic plant comprising plant cells that exhibit altered responsiveness to the stress condition.

43. The method of claim 42, wherein the stress condition is cold stress, and wherein the polynucleotide portion of a plant stress-regulated gene comprises a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1261, 2704-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, and 3313-3955.

44. The method of claim 42, wherein the stress condition is saline stress, and wherein the polynucleotide portion of a plant stress-regulated gene comprises a nucleotide sequence as set forth in any of SEQ ID NOS:2226-2427 and 4910-5107.

45. The method of claim 42, wherein the stress condition is osmotic stress, and wherein the polynucleotide portion of a plant stress-regulated gene comprises a nucleotide sequence as set forth in any of SEQ ID NOS:2428-2585 and 5108-5263.

46. A method of producing a transgenic plant comprising plant cells that exhibit altered responsiveness to a combination of at least two stress conditions, the method comprising introducing a polynucleotide portion of a plant stress-regulated gene into a plant cell genome, whereby the polynucleotide portion of the plant stress-regulated gene modulates a response of the plant cells to a combination of at least two stress conditions, thereby producing a transgenic plant comprising plant cells that exhibit altered responsiveness to the stress conditions.

47. The method of claim 46, wherein the combination of at least two stress conditions is a combination of cold stress and osmotic stress, and wherein the polynucleotide portion of the plant stress-regulate gene comprises a nucleotide sequences as set forth in any of SEQ ID NOS:1669-1969 and 4389-4654.

48. The method of claim 46, wherein the combination of at least two stress conditions is a combination of cold stress and osmotic stress, and wherein the polynucleotide portion of the plant stress-regulate gene comprises a nucleotide sequences as set forth in any of SEQ ID NOS:1699-1725, 1727-1865, 1867-1917, 1919-1927, 1929-1969, 4389-4414, 4416-4552, 4554-4602, 4604-4612, and 4613-4654.

49. The method of claim 46, wherein the combination of at least two stress conditions is a combination of cold stress and saline stress, and wherein the polynucleotide portion of the plant stress-regulate gene comprises a nucleotide sequences as set forth in any of SEQ ID NOS:1970-2226 and4655-4909.

50. The method of claim 46, wherein the combination of at least two stress conditions is a combination of osmotic stress and saline stress, and wherein the polynucleotide portion of the plant stress-regulate gene comprises a nucleotide sequences as set forth in any of SEQ ID NOS:2586-2703 and 5264-5379.

51. The method of claim 46, wherein the combination of at least two stress conditions is a combination of cold stress, osmotic stress and saline stress, and wherein the polynucleotide portion of the plant stress-regulate gene comprises a nucleotide sequences as set forth in any of SEQ ID NOS:1262-1698 and 3956-4388.

52. The method of claim 46, wherein the combination of at least two stress conditions is a combination of cold stress, osmotic stress and saline stress, and wherein the polynucleotide portion of the plant stress-regulate gene comprises a nucleotide sequences as set forth in any of SEQ ID NOS:1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1698, 3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, and 4326-4388.

53. The method of any of claim 42 to 52, wherein the polynucleotide portion of the plant stress-regulated gene encodes a stress-regulated polypeptide or functional peptide portion thereof.

54. The method of claim 53, wherein the stress-regulated polypeptide or functional peptide portion thereof increases the stress tolerance of the transgenic plant.

55. The method of claim 53, wherein the stress-regulated polypeptide or functional peptide portion thereof decreases the stress tolerance of the transgenic plant.

56. The method of claim 53, wherein the polynucleotide portion of the plant stress-regulated gene is operatively linked to a heterologous promoter.

57. The method of any of claim 42 to 52, wherein the polynucleotide portion of the plant stress-regulated gene comprises a stress-regulated regulatory element.

58. The method of claim 57, wherein, upon introducing the stress-regulated regulatory element into the plant cell, the regulatory element integrates into the plant cell genome in a site-specific manner.

59. The method of claim 58, wherein, upon integrating into the plant cell genome, the regulatory element is operatively linked to a heterologous nucleotide sequence, which can be expressed in response to a stress condition specific for the regulatory element.

60. The method of claim 57, wherein the plant stress-regulated regulatory element is a mutant regulatory element, which is not responsive to the stress condition, whereby upon integrating into the plant cell genome, the mutant regulatory element disrupts an endogenous stress-regulated regulatory element of a plant stress-regulated gene, thereby altering the responsiveness of the plant stress-regulated gene to the stress condition.

61. The method of any of claim 42 to 60, wherein the stress an abiotic stress.

62. The method of claim 61, wherein the abiotic stress is selected from the group consisting of an abnormal level of cold, osmotic pressure, salinity, and a combination thereof.

63. The method of claim 57, wherein the stress-regulated regulatory element is operatively linked to a polynucleotide encoding a detectable marker.

64. A transgenic plant produced by the method of any of claims 42 to 63.

65. A plant cell from the transgenic plant of claim 64, wherein said plant cell exhibits altered responsiveness to the stress condition or stress conditions.

66. A seed produced by the transgenic plant of claim 64.

67. A cDNA or genomic DNA library prepared from the transgenic plant of claim 64, or from a plant cell from said transgenic plant, wherein said plant cell exhibits altered responsiveness to the stress condition.

68. A method for monitoring a population of plants for exposure to a stress condition or combination of stress conditions, the method comprising:

a) introducing into the population of a plants a sentinel plant, wherein said sentinel plant is a transgenic plant of claim 64, which comprises plant cells containing a stress-regulated regulatory element is operatively linked to a polynucleotide encoding a detectable marker; and

b) examining the sentinel plant for expression of the detectable marker, which is indicative of exposure of the population of plants to a stress condition or combination of stress conditions,

thereby monitoring the population of plants for exposure to a stress condition or combination of stress conditions.

69. The method of claim 68, wherein said stress condition or combination of stress conditions is an abiotic stress condition or combination of abiotic stress conditions.

70. The method of claim 68 or 69, wherein said stress condition or combination of stress conditions is cold stress, osmotic stress, saline stress, and a combination thereof.

71. The method of any of claims 68 to 70, wherein the stress condition is a cold stress condition, and wherein the regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:2704-3955.

72. The method of any of claims 68 to 70, wherein the stress condition is a cold stress condition, and wherein the regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:2704-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, and 3313-3955.

73. The method of any of claims 68 to 70, wherein the stress condition is a saline stress condition, and wherein the regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:4910-5107.

74. The method of any of claims 68 to 70, wherein the stress condition is an osmotic stress condition, and wherein the regulatory comprises a nucleotide sequence as set forth in any of SEQ ID NOS:5108-5263.

75. The method of any of claims 68 to 70, wherein the combination of stress conditions is cold stress and osmotic stress, and wherein the regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NO. 4389-4654.

76. The method of any of claim 68 to 70, wherein the combination of stress conditions is a cold stress and an osmotic stress, and wherein the regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:4389-4414, 4416-4552, 4554-4602, 4604-4612, and 4613-4654.

77. The method of any of claims 68 to 70, wherein the combination of stress condition is a cold stress and a saline stress, and wherein the regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:4655-5909.

78. The method of any of claims 68 to 70, wherein the combination of stress conditions is an osmotic stress and a saline stress, and wherein the regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:5264-5379.

79. The method of any of claims 68 to 70, wherein the combination of stress conditions is a cold stress, an osmotic stress, and a saline stress, and wherein the regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:3956-4388.

80. The method of any of claims 68 to 70, wherein the combination of stress conditions is a cold stress, an osmotic stress, and a saline stress, and wherein the regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, and 4326-4388.

81. The method of any of claims 68 to 80, wherein the detectable marker is visibly detectable.

82. The method of any of claims 68 to 80, wherein said detectable marker comprises a luminescent detectable marker.

83. The method of any of claims 68 to 80, wherein said detectable marker comprises a fluorescent detectable marker.

84. The method of claim 83, wherein said fluorescent detectable marker comprises a green fluorescent protein, a yellow fluorescent protein, a cyan fluorescent protein, a red fluorescent protein, or an enhanced or modified form thereof.

85. A method of selecting a plant having an altered resistance to an abiotic stress condition or a combination of abiotic stress conditions, the method comprising:

a) contacting nucleic acid molecules representative of expressed polynucleotides in a plant cell of a plant to be examined for having an altered resistance to an abiotic stress with a nucleic acid probes that selectively hybridizes under stringent conditions to a plant stress-regulated gene comprising a nucleotide sequence as set forth in any of SEQ ID NO:1-5379;

b) detecting a level of selective hybridization of the nucleic acid probes to a nucleic acid molecule representative of an expressed polynucleotide in the plant cell, wherein the level of selective hybridization corresponds to the level of the expressed polynucleotide in the plant cell, which is indicative of resistance of the plant to an abiotic stress; and

c) selecting a plant having a level of expression of a polynucleotide indicative of altered resistance to an abiotic stress condition.

86. The method of claim 85, wherein the abiotic stress condition is cold stress, and wherein the nucleic acid probe comprises at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1-1261 and 2704-3955.

87. The method of claim 85, wherein the abiotic stress condition is cold stress, and wherein the nucleic acid probe comprises at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1261, 2704-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, and 3313-3955.

88. The method of claim 85, wherein the abiotic stress condition is saline stress, and wherein the nucleic acid probe comprises at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2226-2427 and 4910-5107.

89. The method of claim 85, wherein the abiotic stress condition is osmotic stress, and wherein the nucleic acid probe comprises at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2428-2585 and 5108-5263.

90. The method of claim 85, wherein the combination of abiotic stress conditions is a combination of cold stress and osmotic stress, and wherein the nucleic acid probe comprises at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1669-1969 and 4389-4654.

91. The method of claim 85, wherein the combination of abiotic stress conditions is a combination of cold stress and osmotic stress, and wherein the nucleic acid probe comprises at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1699-1725, 1727-1865, 1867-1917, 1919-1927, 1929-1969, 4389-4414, 4416-4552, 4554-4602, 4604-4612, and 4613-4654.

92. The method of claim 85, wherein the combination of abiotic stress conditions is a combination of cold stress and saline stress, and wherein the nucleic acid probe comprises at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1970-2226 and 4655-4909.

93. The method of claim 85, wherein the combination of abiotic stress conditions is a combination of osmotic stress and saline stress, and wherein the nucleic acid probe comprises at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2586-2703 and 5264-5379.

94. The method of claim 85, wherein the combination of abiotic stress conditions is a combination of cold stress, osmotic stress and saline stress, and wherein the nucleic acid probe comprises at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1262-1698 and 3956-4388.

95. The method of claim 85, wherein the combination of abiotic stress conditions is a combination of cold stress, osmotic stress and saline stress, and wherein the nucleic acid probe comprises at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1698, 3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, and 4326-4388.

96. A method of modulating the responsiveness of a plant cell to a stress condition, the method comprising introducing a polynucleotide portion of a plant stress-regulated gene into the plant cell, wherein said gene comprises a nucleotide sequence of a polynucleotide as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379, thereby modulating the responsiveness of the plant cell to a stress condition.

97. The method of claim 96, wherein the responsiveness of the plant cell is increased upon exposure to the stress condition.

98. The method of claim 97, wherein increased responsiveness of the plant cell increases the stress tolerance of the plant cell to the stress condition.

99. The method of claim 96, wherein the responsiveness of the plant cell is decreased upon exposure to the stress condition.

100. The method of claim 99, wherein decreased responsiveness of the plant cell increases the stress tolerance of the plant cell to the stress condition.

101. The method of claim 96, wherein the polynucleotide portion of the plant stress-regulated gene integrates into the genome of the plant cell, thereby modulating the responsiveness of the plant cell to the stress condition.

102. The method of claim 96, wherein the polynucleotide portion of the plant stress-regulated gene encodes a stress-regulated polypeptide or functional peptide portion thereof.

103. The method of claim 102, wherein the stress-regulated polypeptide or functional peptide portion thereof increases the responsiveness of the plant cell to the stress condition.

104. The method of claim 102, wherein the polynucleotide portion of the plant stress-regulated gene is operatively linked to a heterologous promoter.

105. The method of claim 102, wherein the polynucleotide portion of the plant stress-regulated gene contains a mutation, whereby upon integrating into the plant cell genome, the polynucleotide disrupts an endogenous plant stress-regulated gene, thereby modulating the responsiveness of said plant cell to the stress condition.

106. The method of claim 105, wherein the endogenous plant stress-regulated gene encodes a maladaptive stress-regulated polypeptide, and wherein said plant cell exhibits increased tolerance to the stress condition.

107. The method of claim 96, wherein the polynucleotide portion of the plant stress-regulated gene comprises a stress-regulated gene regulatory element.

108. The method of claim 107, wherein, the regulatory element is operatively linked to a heterologous nucleotide sequence, which, upon expression from the regulatory element in response to a stress condition, modulates the responsiveness of the plant cell to the stress condition.

109. The method of claim 108, wherein the heterologous nucleotide sequence encodes a stress-inducible transcription factor.

110. The method of claim 109, wherein the transcription factor is DREB1A.

111. The method of claim 108, wherein the heterologous nucleotide sequence encodes a polynucleotide specific for a plant stress-regulated gene, said polynucleotide selected from the group consisting of an antisense molecule, a ribozyme, and a triplexing agent, which, upon expression in the plant cell, reduces or inhibits expression of a stress-regulated polypeptide encoded by the gene, thereby modulating the responsiveness of the plant cell to a stress condition.

112. The method of claim 108, wherein the heterologous nucleotide sequence encodes a recombinant polypeptide comprising a zinc finger domain and a transcription effector domain.

113. The method of claim 112, wherein the transcription effector domain is a transcription activator domain.

114. The method of claim 96, wherein the stress condition is cold stress, osmotic stress, saline stress, or a combination thereof.

117. A method of expressing a heterologous nucleotide sequence in a plant cell, the method comprising introducing into the plant cell a plant stress-regulated regulatory element operatively linked to the heterologous nucleotide sequence, wherein said regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:2704-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379, whereby, upon exposure of the plant cell to stress condition, the heterologous nucleotide sequence is expressed in the plant cell.

118. The method of claim 117, wherein the heterologous nucleotide sequence encodes a selectable marker.

119. The method of claim 117, wherein the heterologous nucleotide sequence encodes a polypeptide that improves the nutritional value of the plant cell.

120. The method of claim 117, wherein the heterologous nucleotide sequence encodes a polypeptide that improves the ornamental value of the plant cell.

121. A method of modulating the activity of a biological pathway in a plant cell involving a plant stress-regulated polypeptide, the method comprising introducing a polynucleotide portion of a plant stress-regulated gene into the plant cell, wherein the plant stress-regulated gene comprises a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379, thereby modulating the activity of the biological pathway.

122. A plant cell obtained by any of claims 96 to 121.

123. A plant comprising the plant cell of claim 122.

124. A method of identifying a polynucleotide that modulates a stress response in a plant cell, the methods comprising:

a) contacting an array of probes representative of a plant cell genome and nucleic acid molecules expressed in plant cell exposed to the stress;

b) detecting a nucleic acid molecule that is expressed at a level different from a level of expression in the absence of the stress;

c) introducing the nucleic acid molecule of step b) into a plant cell; and

d) detecting a modulated response of the plant cell of step c) to a stress, thereby identifying a polynucleotide that modulates a stress response in a plant cell.

125. The method of claim 124, wherein the stress is an abiotic stress.

126. The method of claim 125, wherein the abiotic stress is selected from the group consisting of an abnormal level of cold, osmotic pressure, and salinity.

127. The method of claim 124, wherein expression of the nucleic acid molecule increases the tolerance of the plant cell to the stress.

128. The method of claim 124, wherein, in step b), the nucleic acid molecule is expressed at a level that is less than the level of expression in the absence of the stress.

129. A transgenic plant, which contains a transgene comprising a polynucleotide portion of plant stress-regulated gene, wherein the gene comprises a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379.

130. The transgenic plant of claim 129, wherein the transgenic plant exhibits altered responsiveness to a stress condition as compared to a corresponding wild-type plant.

131. The transgenic plant of claim 130, wherein the transgene disrupts an endogenous stress-regulated gene in the plant, thereby reducing or inhibiting expression of the gene in response to a stress condition.

132. The transgenic plant of claim 130, wherein the plant exhibits increased tolerance to a stress condition.

133. The transgenic plant of claim 130, wherein the plant exhibits decreased tolerance to a stress condition.

134. The transgenic plant of any of claims 129 to 133, wherein the transgene comprises a coding sequence of a plant stress-regulated gene.

135. The transgenic plant of claim 134, wherein the coding sequence is operatively linked to a heterologous regulatory element.

136. The transgenic plant of claim 135, wherein the regulatory element is a constitutively active regulatory element.

137. The transgenic plant of claim 135, wherein the regulatory element is an regulated regulatory element.

138. The transgenic plant of claim 135, wherein the regulatory element is a tissue specific or phase specific regulatory element.

139. The transgenic plant of any of claims 129 to 131, wherein the transgene comprises a plant stress-regulated regulatory element operatively linked to a heterologous nucleotide sequence.

140. The transgenic plant of claim 139, wherein the transgenic plant expresses a polypeptide encoded by the heterologous nucleotide sequence.

141. The transgenic plant of claim 140, wherein the polypeptide improves the nutritional value or ornamental value of the plant.

142. The transgenic plant of any of claims 129 to 141, wherein the plant comprises multiple transgenes.

143. The transgenic plant of claim 142, wherein the multiple transgenes comprise multiple copies of the same transgene or comprise two or more different transgenes.

144. A plant stress-regulated gene regulatory element, wherein the gene comprises a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379.

145. The plant stress-regulated gene regulatory element of claim 144, comprising a nucleotide sequence as set forth in any of SEQ ID NOS: 2704-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3513-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279,, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, 4604-4612, and 4614-5379, or a nucleotide sequence substantially similar thereto.

146. A method of identifying an agent that modulates the activity of the plant stress-regulated regulatory element of claim 144 or claim 145, the method comprising:

a) contacting the regulatory element with an agent suspected of having the ability to modulate the activity of the regulatory element; and

b) detecting a change in the activity of the regulatory element, thereby identifying an agent that modulates the activity of the plant stress-regulated regulatory element.

147. The method of claim 146, wherein the regulatory element can be operatively linked to a heterologous nucleotide sequence.

148. The method of claim 147, wherein the heterologous nucleotide sequence encodes a reporter molecule.

149. The method of any of claims 146 to 148, which is *in vitro* in a plant cell-free system, in a plant cell in culture, or in a plant *in situ*.

150. The method of claim 149, wherein the plant is a transgenic plant, into which the plant stress-regulated regulatory element has been introduced.

151. The method of any of claims 146 to 150, wherein the agent is a stress mimic.

152. A method of modulating a stress-regulated response in a plant cell, the method comprising expressing in the plant cell a recombinant polypeptide that interacts specifically with a plant stress-regulated regulatory element of claim 144 or claim 145, thereby modulating a stress-regulated response in the plant.

153. The method of claim 152, wherein the recombinant polypeptide comprises a zinc finger domain, which specifically interacts with the stress-regulated regulatory element, and a transcription effector domain, which effects expression of the regulatory element.

154. The method of claim 153, wherein the effector domain is a transcription activation domain.

155. The method of claim 153, wherein the effector domain is a transcription repressor domain.

156. A method for identifying a polynucleotide involved in a stress response of a plant, the method comprising:

a) contacting nucleic acid molecules representative of expressed polynucleotides in plant cells of a plant exposed to a stress condition or combination of stress conditions with an array of probes representative of the plant cell genome; and

b) detecting a nucleic acid molecule that exhibits at least a two-fold change in the level of expression as compared to the level of the nucleic acid molecule in a corresponding plant cell of a plant that was not exposed to the stress condition, thereby identifying a polynucleotide involved in a stress response of the plant.

157. The method of claim 156, comprising identifying a plurality of polynucleotides involved in the stress response in the plant.

158. The method of claim 156 or 157, further comprising isolating the polynucleotide or plurality of polynucleotides.

159. A computer readable medium having stored thereon computer executable instructions for performing a method comprising:

a) receiving data on expression in a cell of a plant of a nucleic acid molecule having at least 70% sequence identity to a nucleotide sequence comprising any of SEQ ID NO. 1-5379; and

b) comparing the data on expression of the nucleic acid molecule with data on expression of the nucleic acid in a cell of a plant that has not been exposed to an abiotic stress, of a plant that has been exposed to an abiotic stress condition or combination of abiotic stress conditions, or of a combination of such plants.

160. The computer readable medium of claim 159, wherein the nucleic acid molecule comprises one of a plurality of nucleic acid molecules, and wherein the computer executable instructions are capable performing receiving and comparing of any or all of the plurality of nucleic acid molecules.

161. A computer-readable medium having stored thereon a data structure comprising:

sequence data for at least one nucleic acid molecule having at least 70% nucleic acid sequence identity to a polynucleotide having a nucleotide sequence as set forth in any of SEQ ID NO. 1-5379 or a nucleotide sequence complementary thereto; and

a module receiving the nucleic acid molecule sequence data, which compares the nucleic acid molecule sequence data to a least one other nucleic acid sequence.